

A. Kubelik

Re-run

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#5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,593

DATE: 12/06/2002
TIME: 17:44:19

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\12062002\J047593.raw

4 <110> APPLICANT: Crane, Edmund H. III
5 Rice, Douglas A.
7 <120> TITLE OF INVENTION: Maize NPR1 Polynucleotides and Methods
8 of Use
10 <130> FILE REFERENCE: 1090D2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,593
C--> 12 <141> CURRENT FILING DATE: 2002-01-15
12 <150> PRIOR APPLICATION NUMBER: 60/130,692
13 <151> PRIOR FILING DATE: 1999-04-23
15 <150> PRIOR APPLICATION NUMBER: 09/551,778
16 <151> PRIOR FILING DATE: 2000-04-18
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2154
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (67)...(1929)
31 <221> NAME/KEY: 3'UTR
32 <222> LOCATION: (1933)...(2154)
W--> 34 <221> 5'UTR
35 <222> LOCATION: (1)...(66)
W--> 37 <400> 1

38 gtcgtatgg tccgggtccg gcacaagtag gggctcgctgt cttgcgccttgcagttgtgg 60
39 gaagcc atg gag ccg tcg tcg tcc atc acg ttc gcg tcg tcg tcg tcg 108
40 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser
41 1 5 10
43 tac ctg tcc aac ggc tcg agc ccc tgt tcc gtc gcg ctg ccg ccg cca 156
44 Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro
45 15 20 25 30
47 ggg ccg ccc cag act ccc ccg ttg cct gcc ggc cag ggg tgg ggt ggt 204
48 Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly
49 35 40 45
51 gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg 252
52 Gly Val Ala Ala Ala Gly Ser Gly Ser Val Glu Ala Val Ser Leu
53 50 55 60
55 aac ccg ctc agc aaa aac ctc gag ccg ctg ctc ctc gac ccg gac cta 300
56 Asn Arg Leu Ser Lys Asn Leu Glu Arg Leu Leu Asp Pro Asp Leu
57 65 70 75
59 gac tgc agc gac gcc gac gtc gat gtg ccc gac ggt ggg ccg ccc gta 348
60 Asp Cys Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val

ENTERED

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61	80	85	90	
63	ccc atc cac cgc tgc atc ctt gcc gca cgc agc gac ttc ttc tac gac			396
64	Pro Ile His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp			
65	95	100	105	110
67	ctc ttc gcc gct cgc ggc cgc gca ggg gca gcg cgc ggt gat gcg gcc			444
68	Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala			
69	115	120	125	
71	gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg cgg			492
72	Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg			
73	130	135	140	
75	tac aag atg gag gat ctc gtt ccc gcc ggc cgc gtg ggg cgc gag gcc			540
76	Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala			
77	145	150	155	
79	ttc cag gcg ttt ctg ggg tac ctg tac acc ggc aag ctc ccg ccg gca			588
80	Phe Gln Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala			
81	160	165	170	
83	ccg gtc gac gtg gtg tct tgt gct gac cca gtg tgc cat cac gat tcg			636
84	Pro Val Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser			
85	175	180	185	190
87	tgc ccg ccg gcc atc agg tcc gcg gtc gag ctc atg tac gct gcg gct			684
88	Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys			
89	195	200	205	
91	acc ttc aag atc ccc gag ctc acc tcg ctc ttc cag cgc ccg ctt ctt			732
92	Thr Phe Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu			
93	210	215	220	
95	aat ttt gta gac aag act cta gtg gag gat gtt att cct att ctg gaa			780
96	Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu			
97	225	230	235	
99	gtt gct tcc cac tca ggg ctg act caa gtg atc gac aaa tgt att caa			828
100	Val Ala Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln			
101	240	245	250	
103	agg att gct aga tca gat ctc gac gat ata tct ttg gat aag gag ctc			876
104	Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu			
105	255	260	265	270
107	cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa			924
108	Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln			
109	275	280	285	
111	act gct gat ggt gat acg ttc att tcg gac cct gtg cat gag aaa aga			972
112	Thr Ala Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg			
113	290	295	300	
115	gtc aga aga atc cac agg gca ctt gac tct gat gat gtt gag ctt gtg			1020
116	Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val			
117	305	310	315	
119	aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca			1068
120	Lys Leu Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala			
121	320	325	330	
123	tta cac tat gct gct tac tgt gat gat cct aaa gtt gtc tca gag ctg			1116
124	Leu His Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu			
125	335	340	345	350

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127	tta	aat	ttg	gca	atg	gct	aac	tta	aat	ttg	aag	aat	agc	cgt	ggg	tac	1164
128	Leu	Asp	Leu	Ala	Met	Ala	Asn	Leu	Asn	Leu	Lys	Asn	Ser	Arg	Gly	Tyr	
129					355					360					365		
131	aca	gca	ctc	cac	ttg	gct	gtt	atg	agg	aga	gaa	cca	gct	ata	atc	atg	1212
132	Thr	Ala	Leu	His	Leu	Ala	Ala	Met	Arg	Arg	Glu	Pro	Ala	Ile	Ile	Met	
133					370				375					380			
135	tgt	ctc	ctt	aac	aaa	ggg	gca	aat	gtg	tca	caa	ctg	aca	gct	gat	ggc	1260
136	Cys	Leu	Leu	Asn	Lys	Gly	Ala	Asn	Val	Ser	Gln	Leu	Thr	Ala	Asp	Gly	
137					385				390					395			
139	agg	agc	gca	att	ggt	att	tgt	cgg	agg	tta	aca	aga	gca	aaa	gac	tac	1308
140	Arg	Ser	Ala	Ile	Gly	Ile	Cys	Arg	Arg	Leu	Thr	Arg	Ala	Lys	Asp	Tyr	
141					400				405					410			
143	aat	aca	aag	atg	gag	cag	ggt	caa	gaa	tca	aat	aaa	gat	agg	ctg	tgt	1356
144	Asn	Thr	Lys	Met	Glu	Gln	Gly	Gln	Glu	Ser	Asn	Lys	Asp	Arg	Leu	Cys	
145					415				420					425			430
147	ata	gat	att	cta	gag	agg	gag	atg	atg	cgg	aat	cct	atg	gcg	gtg	gaa	1404
148	Ile	Asp	Ile	Leu	Glu	Arg	Glu	Met	Met	Arg	Asn	Pro	Met	Ala	Val	Glu	
149					435				440					445			
151	gat	gcc	gtc	acc	tcg	cct	ttg	ttg	gca	gat	gat	ctt	cac	atg	aag	ctt	1452
152	Asp	Ala	Val	Thr	Ser	Pro	Leu	Leu	Ala	Asp	Asp	Leu	His	Met	Lys	Leu	
153					450				455					460			
155	ctc	tac	ctg	gaa	aac	aga	gtt	gca	ttt	gct	aga	ttg	ttc	ttt	cct	gct	1500
156	Leu	Tyr	Leu	Glu	Asn	Arg	Val	Ala	Phe	Ala	Arg	Leu	Phe	Phe	Pro	Ala	
157					465				470					475			
159	gaa	gcc	aag	gtc	gcc	atg	caa	atc	gca	caa	gca	gac	acc	aca	gaa	gaa	1548
160	Glu	Ala	Lys	Val	Ala	Met	Gln	Ile	Ala	Gln	Ala	Asp	Thr	Thr	Glu	Glu	
161					480				485					490			
163	tcc	ggc	ggt	ata	gtt	gca	gtt	gca	gca	agc	act	tct	ggt	aaa	ctg	agg	1596
164	Phe	Gly	Gly	Ile	Val	Ala	Val	Ala	Ala	Ser	Thr	Ser	Gly	Lys	Leu	Arg	
165					495				500					505			510
167	gag	gtg	gac	ctt	aat	gag	acg	cca	gtg	aca	caa	aac	aaa	agg	ctc	cgt	1644
168	Glu	Val	Asp	Leu	Asn	Glu	Thr	Pro	Val	Thr	Gln	Asn	Lys	Arg	Leu	Arg	
169					515				520					525			
171	tca	agg	gta	aat	gat	gca	ctg	atg	aaa	aca	gtg	gag	ctg	ggc	cgt	cggt	1692
172	Ser	Arg	Val	Asp	Ala	Leu	Met	Lys	Thr	Val	Glu	Leu	Gly	Arg	Arg	Tyr	
173					530				535					540			
175	tcc	ccg	aac	tgc	tcg	cag	gtt	ctg	gac	aag	ttc	ctg	gag	gac	gat	ctg	1740
176	Phe	Pro	Asn	Cys	Ser	Gln	Val	Leu	Asp	Lys	Phe	Leu	Glu	Asp	Asp	Leu	
177					545				550					555			
179	ccg	gaa	ggg	ctg	gac	cag	ttc	tac	ctc	cag	agg	ggc	aca	gcc	gat	gag	1788
180	Pro	Glu	Gly	Leu	Asp	Gln	Phe	Tyr	Leu	Gln	Arg	Gly	Thr	Ala	Asp	Glu	
181					560				565					570			
183	cag	aag	gtg	aag	agg	atg	cgc	ttc	tgc	gag	ctg	aaa	gag	gac	gtg	ctg	1836
184	Gln	Lys	Val	Lys	Arg	Met	Arg	Phe	Cys	Glu	Leu	Lys	Glu	Asp	Val	Leu	
185					575				580					585			590
187	aag	gct	ttt	agc	aag	gac	aag	gct	gag	ggc	agc	gtg	ttc	tcg	ggc	ctg	1884
188	Lys	Ala	Phe	Ser	Lys	Asp	Lys	Ala	Glu	Gly	Ser	Val	Phe	Ser	Gly	Leu	
189					595				600					605			
191	tcc	tcg	tcg	tcg	tgc	tgc	ccg	ccc	cag	aag	tat	gcc	cag	aaq		1929	

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192 Ser Ser Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
 193 610 615 620
 195 tgatcaaggc accagttttt gccgtatagt ttgttatcat ggtcttcgag acttggaccc 1989
 196 ggacagcata tagggacatg tacaccctgtg tatgtatagt gcttacaatt ggcgtaagta 2049
 197 gaactatatg tatgaacat aaggaaacat ggcaggaaca ccgtgcaaaa agatgaaaag 2109
 198 atggccgaag tgctctatgc gaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 2154
 200 <210> SEQ ID NO: 2
 201 <211> LENGTH: 621
 202 <212> TYPE: PRT
 203 <213> ORGANISM: Zea mays
 205 <400> SEQUENCE: 2
 206 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
 207 1 5 10 15
 208 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
 209 20 25 30
 210 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Val
 211 35 40 45
 212 Ala Ala Ala Gly Ser Gly Ser Val Glu Ala Val Ser Leu Asn Arg
 213 50 55 60
 214 Leu Ser Lys Asn Leu Glu Arg Leu Leu Asp Pro Asp Leu Asp Cys
 215 65 70 75 80
 216 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
 217 85 90 95
 218 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
 219 100 105 110
 220 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Gly
 221 115 120 125
 222 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
 223 130 135 140
 224 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
 225 145 150 155 160
 226 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
 227 165 170 175
 228 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
 229 180 185 190
 230 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
 231 195 200 205
 232 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
 233 210 215 220
 234 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
 235 225 230 235 240
 236 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
 237 245 250 255
 238 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
 239 260 265 270
 240 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
 241 275 280 285
 242 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
 243 290 295 300

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244 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
 245 305 310 315 320
 246 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
 247 325 330 335
 248 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
 249 340 345 350
 250 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
 251 355 360 365
 252 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
 253 370 375 380
 254 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
 255 385 390 395 400
 256 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
 257 405 410 415
 258 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
 259 420 425 430
 260 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
 261 435 440 445
 262 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
 263 450 455 460
 264 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
 265 465 470 475 480
 266 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
 267 485 490 495
 268 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
 269 500 505 510
 270 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
 271 515 520 525
 272 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
 273 530 535 540
 274 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
 275 545 550 555 560
 276 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
 277 565 570 575
 278 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
 279 580 585 590
 281 Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
 283 595 600 605
 285 Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
 287 610 615 620
 288 <210> SEQ ID NO: 3
 289 <211> LENGTH: 7789
 290 <212> TYPE: DNA
 291 <213> ORGANISM: Zea mays
 293 <220> FEATURE:
 294 <221> NAME/KEY: promoter
 295 <222> LOCATION: (1)...(2715)
 297 <221> NAME/KEY: 5'UTR
 298 <222> LOCATION: (2716)...(2781)

VERIFICATION SUMMARY
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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\12062002\J047593.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:37 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:300 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:303 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:306 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:309 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:312 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:315 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:318 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:324 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3